

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Max-Planck-Gesellschaft zur Förderung der
Wissenschaften e.V.
 (B) STREET: none
 (C) CITY: Berlin
 (E) COUNTRY: DE
 (F) POSTAL CODE (ZIP): none

(ii) TITLE OF INVENTION: Nucleic acid molecules encoding an
RNA-directed RNA polymerase (RdRP)

(iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3731 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tomato

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 194..3535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAAATATTCT TTACTTACTT CACCAGGGAT TGACTCATCA CTCCCTCAA GTCTTTGTGT
60

GTTGTGATAA TAAATTGGT TGTGCTTCAG TTTCAGTCAC TACTGCTGGG TAGTTTTAT
120

TTTGCATAAC TTCAGGGGGT ATTCCAGTTG GTGTTAGCAT TTGAAAGTCG
AACTGCACTT 180

GGAATTTGGC TAC ATG GGA AAG ACA ATT CAG GTT TIC GGA TTC CCT TAT
Met Gly Lys Thr Ile Gln Val Phe Gly Phe Pro Tyr

1 5 10

229

CTT CTC TCT GCG GAA GTG GTT AAG TCA TTC TTA GAG AAA TAT ACA GGA 277
 Leu Leu Ser Ala Glu Val Val Lys Ser Phe Leu Glu Lys Tyr Thr Gly
 15 20 25

TAT GGA ACT GTA TGT GCA TTG GAG GTT AAA CAG TCC AAA GGA GGA TCT 325
 Tyr Gly Thr Val Cys Ala Leu Glu Val Lys Gln Ser Lys Gly Gly Ser
 30 35 40

AGA GCA TTT GCC AAA GTT CAA TTT GCC GAC AAC ATA AGT GCT GAC AAA 373
 Arg Ala Phe Ala Lys Val Gln Phe Ala Asp Aan Ile Ser Ala Asp Lys
 45 50 55 60

ATC ATC ACT TTG GCT AAT AAC AGG CTG TAT TTT GGC TCT TCT TAT TTG 421
 Ile Ile Thr Leu Ala Aan Aan Arg Leu Tyr Phe Gly Ser Ser Tyr Leu
 65 70 75

AAG GCT TGG GAA ATG AAA ACT GAT ATT GTC CAA CTG CGG GCA TAT GTG 469
 Lys Ala Trp Glu Met Lys Thr Asp Ile Val Gln Leu Arg Ala Tyr Val
 80 85 90

GAT CAG ATG GAT GGC ATA ACT TTG AAT TTC GGA TGT CAG ATA TCA GAT 517
 Asp Gln Met Asp Gly Ile Thr Leu Asn Phe Gly Cys Gln Ile Ser Asp
 95 100 105

GAC AAG TTT GCA GTG TTG GGA AGT ACA GAA GTT TCA ATT CAA TTT GGC 565
 Asp Lys Phe Ala Val Leu Gly Ser Thr Glu Val Ser Ile Gln Phe Gly
 110 115 120

ATT GGA TTG AAG AAA TTT TTT TTC TTT TTA TCT AGT GGT TCA GCT GAC 613
 Ile Gly Leu Lys Lys Phe Phe Phe Leu Ser Ser Gly Ser Ala Asp
 125 130 135 140

TAT AAA CTT CAG CTT TCA TAT GAA AAT ATA TGG CAG GTT GTG CTC CAT 661
 Tyr Lys Leu Gln Leu Ser Tyr Glu Aan Ile Trp Gln Val Val Leu His
 145 150 155

CGT CCA TAT GGT CAA AAT GCT CAG TTT CTC CTC ATA CAG TTA TTT GGT 709
 Arg Pro Tyr Gly Gln Aan Ala Gln Phe Leu Leu Ile Gln Leu Phe Gly
 160 165 170

GCT CCT CGG ATC TAT AAG AGA CTT GAA AAC TCC TGT TAT AGC TTC TTT 757
 Ala Pro Arg Ile Tyr Lys Arg Leu Glu Aan Ser Cys Tyr Ser Phe Phe
 175 180 185

AAG GAA ACT CCT GAT GAT CAG TGG GTG AGG ACA ACA GAT TTC CCT CCA 805
 Lys Glu Thr Pro Asp Asp Gln Trp Val Arg Thr Thr Asp Phe Pro Pro
 190 195 200

TCT TGG ATA GGG CTA TCT TCT AGC TTA TGT TTG CAG TTC CGT AGG GGT 853
 Ser Trp Ile Gly Leu Ser Ser Leu Cys Leu Gln Phe Arg Arg Gly
 205 210 215 220

GTT CGT CTT CCA AAT TTC GAG GAA AGT TTT TTC CAC TAT GCA GAA CGT 901
 Val Arg Leu Pro Aan Phe Glu Glu Ser Phe Phe His Tyr Ala Glu Arg
 225 230 235

GAA AAC AAT ATT ACT TTA CAG ACT GGT TTC ACC TTT TTC GTC TCT CAA 949
 Glu Asn Aan Ile Thr Leu Gln Thr Gly Phe Thr Phe Phe Val Ser Gln

240 245 250

AAA TCG GCT CTG GTT CCC AAT GTC CAG CCT CCG GAA GGA ATT TCA ATT 997
 Lys Ser Ala Leu Val Pro Asn Val Gln Pro Pro Glu Gly Ile Ser Ile
 255 - - 260 265

CCC TAC AAG ATT TTG TTC AAA ATT AGT TCT TTG GTA CAG CAT GGA TGC 1045
 Pro Tyr Lys Ile Leu Phe Lys Ile Ser Ser Leu Val Gln His Gly Cys
 270 275 280

ATA CCT GGG CCA GCA TTA AAT GTC TAC TTT TTC CGA TTA GTT GAT CCT 1093
 Ile Pro Gly Pro Ala Leu Asn Val Tyr Phe Phe Arg Leu Val Asp Pro
 285 290 295 300

CGA AGG AGA AAT GTG GCA TGC ATT GAG CAT GCC TTA GAG AAA CTG TAC 1141
 Arg Arg Arg Asn Val Ala Cys Ile Glu His Ala Leu Glu Lys Leu Tyr
 305 310 315

TAT ATA AAG GAG TGC TGT TAT GAT CCC GTG AGG TGG CTC ACT GAG CAG 1189
 Tyr Ile Lys Glu Cys Cys Tyr Asp Pro Val Arg Trp Leu Thr Glu Gln
 320 325 330

TAT GAT GGG TAT CTC AAG GGT AGA CAA CCT CCA AAA TCT CCG TCC ATC 1237
 Tyr Asp Gly Tyr Leu Lys Gly Arg Gln Pro Pro Lys Ser Pro Ile
 335 340 345

ACT TTA GAT GAT GGG TTG GTG TAT GTA AGA AGG GTC CTA GTA ACA CCA 1285
 Thr Leu Asp Asp Gly Leu Val Tyr Val Arg Arg Val Leu Val Thr Pro
 350 355 360

TGC AAA GTT TAT TTT TGT GGT CCA GAG GTT AAT GTT TCC AAT CGG GTT 1333
 Cys Lys Val Tyr Phe Cys Gly Pro Glu Val Asn Val Ser Asn Arg Val
 365 370 375 380

CTC CGC AAT TAT TCT GAA GAC ATA GAT AAC TTT CTT CGT GTT TCT TTT 1381
 Leu Arg Asn Tyr Ser Glu Asp Ile Asp Asn Phe Leu Arg Val Ser Phe
 385 390 395

GTT GAT GAG GAG TGG GAG AAA CTG TAT TCT ACA GAC TTA TTA CCA AAA 1429
 Val Asp Glu Glu Trp Glu Lys Leu Tyr Ser Thr Asp Leu Leu Pro Lys
 400 405 410

GCA AGT ACT GGA AGT GGT GTC AGG ACA AAC ATC TAT GAG AGG ATC TTA 1477
 Ala Ser Thr Gly Ser Gly Val Arg Thr Asn Ile Tyr Glu Arg Ile Leu
 415 420 425

TCA ACT CTG CGG AAA GGC TTT GTA ATT GGT GAT AAA AAA TTT GAA TTT 1525
 Ser Thr Leu Arg Lys Gly Phe Val Ile Gly Asp Lys Lys Phe Glu Phe
 430 435 440

CTT GCA TTT TCA TCG AGC CAG TTG CGG GAT AAT TCA GTG TGG ATG TTT 1573
 Leu Ala Phe Ser Ser Gln Leu Arg Asp Asn Ser Val Trp Met Phe
 445 450 455 460

GCA TCA AGA CCT GGC CTT ACT GCA AAT GAT ATA AGA GCT TGG ATG GGT 1621
 Ala Ser Arg Pro Gly Leu Thr Ala Asn Asp Ile Arg Ala Trp Met Gly
 465 470 475

GAT TTT TCG CAG ATC AAG AAT GTC GCA AAA TAT GCT GCC AGA CTT GGT 1669
 Asp Phe Ser Gln Ile Lys Asn Val Ala Lys Tyr Ala Ala Arg Leu Gly
 480 485 490

CAA TCT TTT GGT TCC TCC AGA GAG ACT TTG AGT GTT CTT AGG CAT GAG 1717
 Gln Ser Phe Gly Ser Ser Arg Glu Thr Leu Ser Val Leu Arg His Glu
 495 500 505

ATT GAA GTT ATT CCC GAT GTA AAG GTT CAT GGA ACC AGC TAT GTC TTT 1765
 Ile Glu Val Ile Pro Asp Val Lys Val His Gly Thr Ser Tyr Val Phe
 510 515 520

TCT GAT GGA ATT GGT AAA ATA TCT GGT GAC TTT GCT CAT AGA GTT GCC 1813
 Ser Asp Gly Ile Gly Lys Ile Ser Gly Asp Phe Ala His Arg Val Ala
 525 530 535 540

TCA AAA TGT GGC CTT CAA TAT ACC CCA TCT GCT TTC CAG ATT CGT TAT 1861
 Ser Lys Cys Gly Leu Gln Tyr Thr Pro Ser Ala Phe Gln Ile Arg Tyr
 545 550 555

GGT GGA TAT AAA GGT GTT GTG GGT GTT GAT CCG GAT TCA TCA ATG AAG 1909
 Gly Gly Tyr Lys Gly Val Val Gly Val Asp Pro Asp Ser Ser Met Lys
 560 565 570

TTG TCT TTG AGA AAG AGC ATG TCG AAA TAT GAA TCA GAC AAC ATA AAG 1957
 Leu Ser Leu Arg Lys Ser Met Ser Lys Tyr Glu Ser Asp Asn Ile Lys
 575 580 585

TTA GAT GTC CTT GGA TGG AGC AAA TAT CAG CCT TGT TAT CTT AAT CGT 2005
 Leu Asp Val Leu Gly Trp Ser Lys Tyr Gln Pro Cys Tyr Leu Asn Arg
 590 595 600

CAA CTG ATT ACG CTC TTG TCT ACA CTT GGA GTG AAA GAT GAA GTT CTC 2053
 Gln Leu Ile Thr Leu Leu Ser Thr Leu Gly Val Lys Asp Glu Val Leu
 605 610 615 620

GAA CAG AAG CAA AAG GAA GCT GTA GAT CAG CTT GAT GCT ATC TTG CAT 2101
 Glu Gln Lys Gln Lys Glu Ala Val Asp Gln Leu Asp Ala Ile Leu His
 625 630 635

GAT TCT TTG AAG GCA CAG GAG GCT TTG GAA TTG ATG TCT CCT GGA GAG 2149
 Asp Ser Leu Lys Ala Gln Glu Ala Leu Glu Leu Met Ser Pro Gly Glu
 640 645 650

AAC ACT AAT ATT CTC AAG GCA ATG CTA AAC TGT GGT TAT AAG CCT GAT 2197
 Asn Thr Asn Ile Leu Lys Ala Met Leu Asn Cys Gly Tyr Lys Pro Asp
 655 660 665

GCT GAG CCC TTT CTT TCA ATG ATG TTG CAA ACC TTC CGC GCA TCC AAG 2245
 Ala Glu Pro Phe Leu Ser Met Met Leu Gln Thr Phe Arg Ala Ser Lys
 670 675 680

TTG CTC GAT TTG CGG ACT AGA TCA AGA ATA TTT ATT CCA AAT GGA AGA 2293
 Leu Leu Asp Leu Arg Thr Arg Ser Arg Ile Phe Ile Pro Asn Gly Arg
 685 690 695 700

ACA ATG ATG GGA TGT TTG GAT GAA TCC AGA ACC TTG GAA TAT GGT CAG 2341
 Thr Met Met Gly Cys Leu Asp Glu Ser Arg Thr Leu Glu Tyr Gly Gln

705 710 715

GTG TTT GTT CAG TTT ACT GGT GCT GGA CAT GGA GAG TTT TCT GAC GAT 2389
 Val Phe Val Gln Phe Thr Gly Ala Gly His Gly Glu Phe Ser Asp Asp
 720 725 730

TTA CAT CCA TTT AAT AAC AGC AGA TCC ACC AAC AGT AAT TTC ATT CTG 2437
 Leu His Pro Phe Asn Asn Ser Arg Ser Thr Asn Ser Asn Phe Ile Leu
 735 740 745

AAG GGA AAT GTG GTT GCA AAA AAT CCA TGC TTG CAT CCT GGT GAT 2485
 Lys Gly Asn Val Val Ala Lys Asn Pro Cys Leu His Pro Gly Asp
 750 755 760

ATT CGT GTT TTA AAG GCT GTA AAT GTT CGA GCG CTG CAC CAC ATG GTA 2533
 Ile Arg Val Leu Lys Ala Val Asn Val Arg Ala Leu His His Met Val
 765 770 775 780

GAT TGT GTT GTA TTC CCT CAG AAA GGA AAA AGA CCT CAT CCG AAT GAA 2581
 Asp Cys Val Val Phe Pro Gln Lys Gly Lys Arg Pro His Pro Asn Glu
 785 790 795

TGT TCT GGG AGT GAT TTG GAT GGG GAT ATC TAC TTT GTT TGC TGG GAT 2629
 Cys Ser Gly Ser Asp Leu Asp Gly Asp Ile Tyr Phe Val Cys Trp Asp
 800 805 810

CAA GAC ATG ATC CCG CCA AGG CAA GTC CAG CCG ATG GAA TAT CCT CCA 2677
 Gln Asp Met Ile Pro Pro Arg Gln Val Gln Pro Met Glu Tyr Pro Pro
 815 820 825

GCA CCC AGC ATA CAG TTG GAC CAT GAT GTC ACA ATT GAG GAA GTT GAA 2725
 Ala Pro Ser Ile Gln Leu Asp His Asp Val Thr Ile Glu Glu Val Glu
 830 835 840

GAG TAC TTC ACC AAC TAT ATT GTG AAT GAC AGT TTG GGA ATC ATA GCA 2773
 Glu Tyr Phe Thr Asn Tyr Ile Val Asn Asp Ser Leu Gly Ile Ile Ala
 845 850 855 860

AAT GCC CAT GTC GTA TTT GCA GAC AGA GAA CCT GAT ATG GCC ATG AGT 2821
 Asn Ala His Val Val Phe Ala Asp Arg Glu Pro Asp Met Ala Met Ser
 865 870 875

GAT CCA TGC AAA AAA CTT GCT GAG CTC TTT TCA ATT GCA GTG GAC TTT 2869
 Asp Pro Cys Lys Lys Leu Ala Glu Leu Phe Ser Ile Ala Val Asp Phe
 880 885 890

CCA AAG ACT GGT GTT CCC GCT GAA ATA CCA TCT CAG TTG CGC CCT AAA 2917
 Pro Lys Thr Gly Val Pro Ala Glu Ile Pro Ser Gin Leu Arg Pro Lys
 895 900 905

GAA TAC CCA GAC TTC ATG GAT AAG CCG GAC AAG ACC AGC TAT ATC TCA 2965
 Glu Tyr Pro Asp Phe Met Asp Lys Pro Asp Lys Thr Ser Tyr Ile Ser
 910 915 920

GAA AGA GTT ATT GGA AAG CTT TTC AGG AAA GTG AAG GAC AAA GCA CCT 3013
 Glu Arg Val Ile Gly Lys Leu Phe Arg Lys Val Lys Asp Lys Ala Pro
 925 930 935 940

CAG GCT AGC TCT ATC GCG ACC TTC ACA AGA GAT GTT GCA AGG AGA TCA 3061
 Gln Ala Ser Ser Ile Ala Thr Phe Thr Arg Asp Val Ala Arg Arg Ser
 945 950 955

TAT GAT GCT GAT ATG GAA GTT GAT GGA TTT GAA GAT TAC ATT GAC GAA 3109
 Tyr Asp Ala Asp Met Glu Val Asp Gly Phe Glu Asp Tyr Ile Asp Glu
 960 965 970

GCT TTT GAC TAC AAA ACT GAA TAT GAC AAC AAG CTG GGT AAT TTA ATG 3157
 Ala Phe Asp Tyr Lys Thr Glu Tyr Asp Asn Lys Leu Gly Asn Leu Met
 975 980 985

GAC TAC TAT GGC ATA AAA ACA GAG GCT GAA ATA CTT AGT GGT GGC ATT 3205
 Asp Tyr Tyr Gly Ile Lys Thr Glu Ala Glu Ile Leu Ser Gly Gly Ile
 990 995 1000

ATG AAG GCA TCA AAA ACT TTT GAC CGC AGA AAA GAT GCT GAG GCC ATT 3253
 Met Lys Ala Ser Lys Thr Phe Asp Arg Arg Lys Asp Ala Glu Ala Ile
 1005 1010 1015 1020

AGT GTT GCT GTG AGG GCC TTG AGG AAG GAG GCA AGA GCA GCC TGG TTC AAG 3301
 Ser Val Ala Val Arg Ala Leu Arg Lys Glu Ala Arg Ala Trp Phe Lys
 1025 1030 1035

AGG CGT AAT GAT ATA GAT GAC ATG TTA CCA AAG GCT TCG GCT TGG TAC 3349
 Arg Arg Asn Asp Ile Asp Asp Met Leu Pro Lys Ala Ser Ala Trp Tyr
 1040 1045 1050

CAC GTT ACA TAT CAT CCT ACA TAT TGG GGT TGC TAC AAT CAG GGG TTG 3397
 His Val Thr Tyr His Pro Thr Tyr Trp Gly Cys Tyr Asn Gln Gly Leu
 1055 1060 1065

AAA AGA GCT CAT TTC ATT AGC TTT CCC TGG TGT GTT TAT GAC CAG CTA 3445
 Lys Arg Ala His Phe Ile Ser Phe Pro Trp Cys Val Tyr Asp Gln Leu
 1070 1075 1080

ATC CAG ATT AAG AAG GAC AAA GCA CGT AAC AGC CCA GTT CTC AAC TTG 3493
 Ile Gin Ile Lys Lys Asp Lys Ala Arg Asn Arg Pro Val Leu Asn Leu
 1085 1090 1095 1100

TCA TCT CTC AGG GCT CAA CTG AGT CAC AGA TTA GTG TTG AAA 3535
 Ser Ser Leu Arg Ala Gin Leu Ser His Arg Leu Val Leu Lys
 1105 1110

TGAGATTCCA GTCGAGCGTT AAGCTGATAT ATATATAATG TAATAGGGTG
 TGATCATAAG 3595

AAA ACT GTTA TGC ATT GTTG ACT ACCTTTT GTCTTTAAAA CTGCATGAAG CTGCAACATA
 3655

TATGCAGTAC TCTAAGAAC AGATGTACAG CTAAGTACTA ATATGTATGT

GATTTGAGTT 3715

TCATCTTCT TCTAAA 3731

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1114 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2;

Met Gly Lys Thr Ile Gln Val Phe Gly Phe Pro Tyr Leu Leu Ser Ala
 1 5 10 15

Glu Val Val Lys Ser Phe Leu Glu Lys Tyr Thr Gly Tyr Gly Thr Val
 20 25 30

Cys Ala Leu Glu Val Lys Gln Ser Lys Gly Gly Ser Arg Ala Phe Ala
 35 40 45

Lys Val Gin Phe Ala Asp Asn Ile Ser Ala Asp Lys Ile Ile Thr Leu
 50 55 60

Ala Asn Asn Arg Leu Tyr Phe Gly Ser Ser Tyr Leu Lys Ala Trp Glu
 65 70 75 80

Met Lys Thr Asp Ile Val Gln Leu Arg Ala Tyr Val Asp Gln Met Asp
 85 90 95

Gly Ile Thr Leu Asn Phe Gly Cys Gln Ile Ser Asp Asp Lys Phe Ala
 100 105 110

Val Leu Gly Ser Thr Glu Val Ser Ile Gln Phe Gly Ile Gly Leu Lys
 115 120 125

Lys Phe Phe Phe Phe Leu Ser Ser Gly Ser Ala Asp Tyr Lys Leu Gln
 130 135 140

Leu Ser Tyr Glu Asn Ile Trp Gln Val Val Leu His Arg Pro Tyr Gly
 145 150 155 160

Gln Asn Ala Gln Phe Leu Leu Ile Gln Leu Phe Gly Ala Pro Arg Ile
 165 170 175

Tyr Lys Arg Leu Glu Asn Ser Cys Tyr Ser Phe Phe Lys Glu Thr Pro
 180 185 190

Asp Asp Gln Trp Val Arg Thr Thr Asp Phe Pro Pro Ser Trp Ile Gly
 195 200 205

Leu Ser Ser Ser Leu Cys Leu Gln Phe Arg Arg Gly Val Arg Leu Pro
 210 215 220

Asn Phe Glu Glu Ser Phe Phe His Tyr Ala Glu Arg Glu Asn Asn Ile
 225 230 235 240

Thr Leu Gln Thr Gly Phe Thr Phe Phe Val Ser Gln Lys Ser Ala Leu
 245 250 255

Val Pro Asn Val Gln Pro Pro Glu Gly Ile Ser Ile Pro Tyr Lys Ile
 260 265 270

Leu Phe Lys Ile Ser Ser Leu Val Gln His Gly Cys Ile Pro Gly Pro
 275 280 285

Ala Leu Asn Val Tyr Phe Phe Arg Leu Val Asp Pro Arg Arg Arg Asn
 290 295 300

Val Ala Cys Ile Glu His Ala Leu Glu Lys Leu Tyr Tyr Ile Lys Glu
 305 310 315 320

Cys Cys Tyr Asp Pro Val Arg Trp Leu Thr Glu Gln Tyr Asp Gly Tyr
 325 330 335

Leu Lys Gly Arg Gln Pro Pro Lys Ser Pro Ser Ile Thr Leu Asp Asp
 340 345 350

Gly Leu Val Tyr Val Arg Arg Val Leu Val Thr Pro Cys Lys Val Tyr
 355 360 365

Phe Cys Gly Pro Glu Val Asn Val Ser Asn Arg Val Leu Arg Asn Tyr
 370 375 380

Ser Glu Asp Ile Asp Asn Phe Leu Arg Val Ser Phe Val Asp Glu Glu
 385 390 395 400

Trp Glu Lys Leu Tyr Ser Thr Asp Leu Leu Pro Lys Ala Ser Thr Gly
 405 410 415

Ser Gly Val Arg Thr Asn Ile Tyr Glu Arg Ile Leu Ser Thr Leu Arg
 420 425 430

Lys Gly Phe Val Ile Gly Asp Lys Lys Phe Glu Phe Leu Ala Phe Ser
 435 440 445

Ser Ser Gln Leu Arg Asp Asn Ser Val Trp Met Phe Ala Ser Arg Pro
 450 455 460

Gly Leu Thr Ala Asn Asp Ile Arg Ala Trp Met Gly Asp Phe Ser Gln
 465 470 475 480

Ile Lys Asn Val Ala Lys Tyr Ala Ala Arg Leu Gly Gln Ser Phe Gly
 485 490 495

Ser Ser Arg Glu Thr Leu Ser Val Leu Arg His Glu Ile Glu Val Ile
 500 505 510

Pro Asp Val Lys Val His Gly Thr Ser Tyr Val Phe Ser Asp Gly Ile
 515 520 525

Gly Lys Ile Ser Gly Asp Phe Ala His Arg Val Ala Ser Lys Cys Gly
 530 535 540

Leu Gln Tyr Thr Pro Ser Ala Phe Gln Ile Arg Tyr Gly Gly Tyr Lys
 545 550 555 560

Gly Val Val Gly Val Asp Pro Asp Ser Ser Met Lys Leu Ser Leu Arg
 565 570 575

Lys Ser Met Ser Lys Tyr Glu Ser Asp Asn Ile Lys Leu Asp Val Leu
 580 585 590

Gly Trp Ser Lys Tyr Gin Pro Cys Tyr Leu Asn Arg Gin Leu Ile Thr
 595 600 605

Leu Leu Ser Thr Leu Gly Val Lys Asp Glu Val Leu Glu Gin Lys Gin
 610 615 620

Lys Glu Ala Val Asp Gln Leu Asp Ala Ile Leu His Asp Ser Leu Lys
 625 630 635 640

Ala Gln Glu Ala Leu Glu Leu Met Ser Pro Gly Glu Asn Thr Asn Ile
 645 650 655

Leu Lys Ala Met Leu Asn Cys Gly Tyr Lys Pro Asp Ala Glu Pro Phe
 660 665 670

Leu Ser Met Met Leu Gln Thr Phe Arg Ala Ser Lys Leu Leu Asp Leu
 675 680 685

Arg Thr Arg Ser Arg Ile Phe Ile Pro Asn Gly Arg Thr Met Met Gly
 690 695 700

Cys Leu Asp Glu Ser Arg Thr Leu Glu Tyr Gly Gln Val Phe Val Gln
 705 710 715 720

Phe Thr Gly Ala Gly His Gly Glu Phe Ser Asp Asp Leu His Pro Phe
 725 730 735

Asn Asn Ser Arg Ser Thr Asn Ser Asn Phe Ile Leu Lys Gly Asn Val
 740 745 750

Val Val Ala Lys Asn Pro Cys Leu His Pro Gly Asp Ile Arg Val Leu
 755 760 765

Lys Ala Val Asn Val Arg Ala Leu His His Met Val Asp Cys Val Val
 770 775 780

Phe Pro Gln Lys Gly Lys Arg Pro His Pro Asn Glu Cys Ser Gly Ser
 785 790 795 800

Asp Leu Asp Gly Asp Ile Tyr Phe Val Cys Trp Asp Gin Asp Met Ile
 805 810 815

Pro Pro Arg Gin Val Gin Pro Met Glu Tyr Pro Pro Ala Pro Ser Ile
 820 825 830

Gln Leu Asp His Asp Val Thr Ile Glu Glu Val Glu Glu Tyr Phe Thr
 835 840 845

Asn Tyr Ile Val Asn Asp Ser Leu Gly Ile Ile Ala Asn Ala His Val
 850 855 860

Val Phe Ala Asp Arg Glu Pro Asp Met Ala Met Ser Asp Pro Cys Lys
 865 870 875 880

Lys Leu Ala Glu Leu Phe Ser Ile Ala Val Asp Phe Pro Lys Thr Gly

885 890 895

Val Pro Ala Glu Ile Pro Ser Gln Leu Arg Pro Lys Glu Tyr Pro Asp
 900 905 910

Phe Met Asp Lys Pro Asp Lys Thr Ser Tyr Ile Ser Glu Arg Val Ile
 915 920 925

Gly Lys Leu Phe Arg Lys Val Lys Asp Lys Ala Pro Gln Ala Ser Ser
 930 935 940

Ile Ala Thr Phe Thr Arg Asp Val Ala Arg Arg Ser Tyr Asp Ala Asp
 945 950 955 960

Met Glu Val Asp Gly Phe Glu Asp Tyr Ile Asp Glu Ala Phe Asp Tyr
 965 970 975

Lys Thr Glu Tyr Asp Asn Lys Leu Gly Asn Leu Met Asp Tyr Tyr Gly
 980 985 990

Ile Lys Thr Glu Ala Glu Ile Leu Ser Gly Gly Ile Met Lys Ala Ser
 995 1000 1005

Lys Thr Phe Asp Arg Arg Lys Asp Ala Glu Ala Ile Ser Val Ala Val
 1010 1015 1020

Arg Ala Leu Arg Lys Glu Ala Arg Ala Trp Phe Lys Arg Arg Asn Asp
 1025 1030 1035 1040

Ile Asp Asp Met Leu Pro Lys Ala Ser Ala Trp Tyr His Val Thr Tyr
 1045 1050 1055

His Pro Thr Tyr Trp Gly Cys Tyr Asn Gln Gly Leu Lys Arg Ala His
 1060 1065 1070

Phe Ile Ser Phe Pro Trp Cys Val Tyr Asp Gln Leu Ile Gln Ile Lys
 1075 1080 1085

Lys Asp Lys Ala Arg Asn Arg Pro Val Leu Asn Leu Ser Ser Leu Arg
 1090 1095 1100

Ala Gln Leu Ser His Arg Leu Val Leu Lys
 1105 1110